GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 24, 2003, 15:46:23 ; Search time 43.8955 Seconds
(without alignments)
1225.145 Million cell updates/sec

Title: US-09-988-971-2
Perfect score: 1351
Sequence: 1 MGSLPSRRKSLPSPSLSSSV.....RESLSFYISLNDEAVSLDDA 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1351	100.0	261	4	Q9H6Q3	Q9h6q3 homo sapien
2	1040	77.0	197	4	Q9H135	Q9h135 homo sapien
3	1032	76.4	259	11	Q8VI42	Q8vi42 mus musculu
4	1023	75.7	259	11	Q8R4L0	Q8r4l0 mus musculu
5	938.5	69.5	210	4	Q8WY18	Q8wy18 homo sapien
6	751.5	55.6	179	11	Q9D1Z9	Q9d1z9 mus musculu
7	495.5	36.7	280	11	Q8QZX8	Q8qzx8 mus musculu
8	495.5	36.7	281	11	Q60898	Q60898 mus musculu
9	485.5	35.9	276	4	Q13239	Q13239 homo sapien
10	370.5	27.4	502	13	Q9DDK6	Q9ddk6 salmo salar
11	365.5	27.1	488	13	O13064	O13064 xenopus lae
12	362.5	26.8	161	4	Q9HBI7	Q9hbi7 homo sapien
13	356.5	26.4	505	4	Q96IN1	Q96in1 homo sapien
14	344	25.5	509	6	Q95M32	Q95m32 hylobates s
15	342.5	25.4	509	11	Q91X65	Q91x65 mus musculu
16	336	24.9	517	5	Q9V9J3	Q9v9j3 drosophila
17	332	24.6	509	6	Q95KR7	Q95kr7 saimiri sci
18	319.5	23.6	537	11	Q62844	Q62844 rattus norv
19	317.5	23.5	496	13	O93411	O93411 xenopus lae
20	313.5	23.2	541	11	Q99PW1	Q99pw1 rattus norv
21	313	23.2	812	15	Q85466	Q85466 y73 sarcoma
22	311	23.0	517	11	Q63206	Q63206 rattus norv
23	310	22.9	534	4	Q16248	Q16248 homo sapien
24	310	22.9	534	6	Q95M31	Q95m31 hylobates s
25	309	22.9	527	5	Q9Y1Z1	Q9y1z1 ephydatia f
26	308.5	22.8	517	5	O77050	O77050 anthocidari
27	306	22.6	63	4	Q96QI4	Q96qi4 homo sapien
28	292.5	21.7	587	15	Q64817	Q64817 avian sarco
29	289	21.4	511	5	Q8WQM5	Q8wqm5 strongyloce
30	288.5	21.4	503	5	Q8WSU5	Q8wsu5 ephydatia f
31	286	21.2	502	13	Q8QGJ9	Q8qgj9 fugu rubrip
32	284.5	21.1	523	15	Q85477	Q85477 rous sarcom
33	284.5	21.1	526	15	Q64994	Q64994 rous sarcom
34	281.5	20.8	526	15	O93080	O93080 rous sarcom
35	280	20.7	535	15	O92957	O92957 rous sarcom
36	279.5	20.7	526	15	Q64993	Q64993 rous sarcom
37	279	20.7	546	15	Q86363	Q86363 rous sarcom
38	277.5	20.5	526	15	O92806	O92806 rous sarcom
39	277.5	20.5	542	11	Q9JJ10	Q9jj10 rattus norv
40	277	20.5	504	5	Q8WSU2	Q8wsu2 ephydatia f
41	277	20.5	545	15	Q86362	Q86362 rous sarcom
42	274.5	20.3	495	5	Q8WSU4	Q8wsu4 ephydatia f
43	273.5	20.2	526	15	Q07461	Q07461 rous sarcom
44	272.5	20.2	526	15	Q60567	Q60567 rous sarcom
45	264.5	19.6	507	5	O45539	O45539 caenorhabdi

ALIGNMENTS

RESULT 1
Q9H6Q3
ID Q9H6Q3 PRELIMINARY; PRT; 261 AA.
AC Q9H6Q3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA: FLJ21992 fis, clone HEP06554 (Src-like adapter protein-2)
DE (Modulator of antigen receptor signaling MARS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21553259; PubMed=11696592;
RA Holland S.J., Liao X.C., Mendenhall M.K., Zhou X., Pardo J., Chu P.,
RA Spencer C., Fu A.C., Sheng N., Yu P., Pali E., Nagin A., Shen M.,
RA Yu S., Chan E., Wu X., Li C., Woisetschlager M., Aversa G.,
RA Kolbinger F., Bennett M.K., Molineaux S., Luo Y., Payan D.G.,
RA Mancebo H.S.Y., Wu J.;
RT "Functional Cloning of Src-like Adapter Protein-2 (SLAP-2), a Novel
RT Inhibitor of Antigen Receptor Signaling.";
RL J. Exp. Med. 194:1263-1276(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Loreto M.P., McGlade C.J.;
RT "Modulator of Antigen Receptor Signaling (MARS).";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AK025645; BAB15201.1; -.

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DR   EMBL; AF326353; AAL29204.1; -.
DR   EMBL; AF290985; AAL38197.1; -.
DR   HSSP; P06239; 1LKK.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   SH3 domain; Receptor.
SQ   SEQUENCE   261 AA;  28585 MW;  858AF03451672B3D CRC64;

  Query Match            100.0%;  Score 1351;  DB 4;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-115;
  Matches  261;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT 60

Qy      61 IVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 IVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120

Qy     121 RESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 RESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELA 180

Qy     181 DDICCLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATGEESLLSEG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DDICCLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATGEESLLSEG 240

Qy     241 LRESLSFYISLNDEAVSLDDA 261
           |||||||||||||||||||||
Db     241 LRESLSFYISLNDEAVSLDDA 261


RESULT 2
Q9H135
ID   Q9H135      PRELIMINARY;      PRT;   197 AA.
AC   Q9H135;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   DJ977B1.1 (Novel protein tyrosine kinase with Src homology domain 2
DE   (SH2) domains) (Fragment).
GN   DJ977B1.1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lloyd D.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL050318; CAB75365.1; -.
DR   HSSP; P06239; 1LKK.
DR   InterPro; IPR000980; SH2.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   PROSITE; PS50001; SH2; 1.
KW   Kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   197 AA;  22124 MW;  EF01FE7A85C5C1F1 CRC64;

  Query Match            77.0%;  Score 1040;  DB 4;  Length 197;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-87;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      65 DGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQ 124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 DGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQ 60

Qy     125 TRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDIC 184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDIC 120

Qy     185 CLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATGEESLLSEGLRES 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATGEESLLSEGLRES 180

Qy     245 LSFYISLNDEAVSLDDA 261
           |||||||||||||||||
Db     181 LSFYISLNDEAVSLDDA 197


RESULT 3
Q8VI42
ID   Q8VI42      PRELIMINARY;      PRT;   259 AA.
AC   Q8VI42;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Modulator of antigen receptor signaling MARS.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Loreto M.P., McGlade C.J.;
RT   "Modulator of Antigen Receptor Signaling (MARS).";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF287467; AAL38196.1; -.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Receptor.
SQ   SEQUENCE   259 AA;  28476 MW;  8270F17CD3FC50A3 CRC64;

  Query Match            76.4%;  Score 1032;  DB 11;  Length 259;
  Best Local Similarity  79.8%;  Pred. No. 3.1e-86;
  Matches  209;  Conservative   16;  Mismatches   33;  Indels    4;  Gaps    3;

Qy       1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT 60
           |||| || |:  ||| |||   | ||:|: || | ||||||||||  | ||||||||||
Db       1 MGSLSSRGKT-SSPSPSSSGPDQEPVSMQPERHKVTAVALGSFPAGEQARLSLRLGEPLT 59

Qy      61 IVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120
           |:|||||||| ||||||||::|||:||||:|||||||||||||||||||||||||||||
Db      60 IISEDGDWWTVQSEVSGREYHMPSVYVAKVAHGWLYEGLSREKAEELLLLPGNPGGAFLI 119

Qy     121 RESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELA 180
           |||||||| ||||||||||||||||||  |||||||||||||||| |||:||||||
Db     120 RESQTRRGCYSLSVRLSRPASWDRIRHYRIQRLDNGWLYISPRLTFPSLHALVEHYSELA 179

Qy     181 DDICCLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEA-ATGEESLLSE 239
           | ||| |:||||||: |||||||  | ||||  : ||||:|| |||| || |:|| |||||
Db     180 DGICCPLREPCVLQKLGPLPGKDTPPPVTVPTSSLNWKKLDRSLLFLEAPASGEASLLSE 239

Qy     240 GLRESLSFYISLNDEAVSLDDA 261
           |||||||  |||| ::   ||||
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Db    240 GLRESLSSYISLAED--PLDDA 259


RESULT 4
Q8R4L0
ID   Q8R4L0      PRELIMINARY;      PRT;   259 AA.
AC   Q8R4L0;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Src-like adapter protein-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pandey A., Ibarrol N., Kratchmarova I., Fernandez M.,
RA   Constantinescu S., Ohara O., Sawasdikosol S., Lodish H.F., Mann M.;
RT   "A novel Src homology 2 domain-containing molecule, Src-Like Adapter
RT   Protein-2 (SLAP-2), which negatively regulates T cell receptor
RT   signaling.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ibarrola N., Mann M., Pandey A.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF434990; AAL86403.1; -.
SQ   SEQUENCE   259 AA;  28516 MW;  1388E68244152E34 CRC64;

  Query Match             75.7%;  Score 1023;  DB 11;  Length 259;
  Best Local Similarity   79.4%;  Pred. No. 2.1e-85;
  Matches  20B;  Conservative   16;  Mismatches   34;  Indels    4;  Gaps    3;

Qy       1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT 60
           |||| || |:  |||| |||   | ||:|: || | ||||||||||  | ||||||||||
Db       1 MGSLSSRGKT-SSPSPSSSGPDQEPVSMQPERHKVTAVALGSFPAGEQAKLSLRLGEPLT 59

Qy      61 IVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120
           |:|||||||| |||||||::|||:||||:|||||||||||||||||||||||||||||||
Db      60 IISEDGDWWTVQSEVSGREYHMPSVYVAKVAHGWLYEGLSREKAEELLLLPGNPGGAFLI 119

Qy     121 RESQTRRGSYSLSVRLSRPASWDR1RHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELA 180
           |||||||| |||||||||||||||||  |||||||| ||||||| |||:||||||
Db     120 RESQTRRGCYSLSVRLSRPASWDRIRHYRIQRLDNGWLYISHRLTFPSLHALVEHYSELA 179

Qy     181 DDICCLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEA-ATGEESLLSE 239
           | ||| |:|||||: ||||||| | ||||  : ||||:|| |||| || |:|| |||||
Db     180 DGICCPLREPCVLQKLGPLPGKDTPPPVTVPTSSLNWKKLDRSLLFLEAPASGEASLLSE 239

Qy     240 GLRESLSFYISLNDEAVSLDDA 261
           ||||||| |||| ::   ||||
Db     240 GLRESLSSYISLAED--PLDDA 259


RESULT 5
Q8WY18
ID   Q8WY18      PRELIMINARY;      PRT;   210 AA.
AC   Q8WY18;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Modulator of antigen receptor signaling, putative splice isoform
DE   MARS-v.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=THYMUS;
RA   Loreto M.P., McGlade C.J.;
RT   "Modulator of Antigen Receptor Signaling (MARS) - putative splice
RT   variant.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF290986; AAL38198.1; -.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Receptor.
SQ   SEQUENCE   210 AA;  23103 MW;  BED62208E53A472E CRC64;

  Query Match             69.5%;  Score 938.5;  DB 4;  Length 210;
  Best Local Similarity   89.4%;  Pred. No. 8.1e-78;
  Matches  185;  Conservative    3;  Mismatches   12;  Indels    7;  Gaps    1;

Qy       1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT 60

Qy      61 IVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 IVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120

Qy     121 RESQTRRGSYSLSVRLSRPASWDR1RHYRIHCLDNGWLYISPRLTFPSLQALVDHYSE-- 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db     121 RESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSEGW 180

Qy     179 -----LADDICCLLKEPCVLQRAGPLP 200
                 |    ::   |:||| ||
Db     181 PAPWQGYTPTCDCAEDTTQLERAGQLP 207


RESULT 6
Q9D1Z9
ID   Q9D1Z9      PRELIMINARY;      PRT;   179 AA.
AC   Q9D1Z9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   A930009E21Rik protein.
GN   A930009E21RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=RETINA;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
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RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK020837; BAB32223.1; -.
DR   HSSP; P06239; 1LKK.
DR   MGD; MGI:1925049; A930009E21Rik.
DR   InterPro; IPR000980; SH2.
DR   Pfam; PF00017; SH2; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   PROSITE; PS50001; SH2; 1.
SQ   SEQUENCE   179 AA;  19926 MW;  60477A0CF4003FCD CRC64;

  Query Match             55.6%;  Score 751.5;  DB 11;  Length 179;
  Best Local Similarity   82.3%;  Pred. No. 8.1e-61;
  Matches  149;  Conservative   11;  Mismatches   18;  Indels    3;  Gaps    2;

Qy      82 IPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPAS 141
           :|||:||||:|||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1 MPSVYVAKVAHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGCYSLSVRLSRPAS 60

Qy     142 WDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQRAGPLPG 201
           |||||||||  |||||||||||||||||| |||:||||||| ||| |:|||||: |||||
Db      61 WDRIRHYRIQRLDNGWLYISPRLTFPSLHALVEHYSELADGICCPLREPCVLQKLGPLPG 120

Qy     202 KDIPLPVTVQRTPLNWKELDSSLLFSEA-ATGEESLLSEGLRESLSFYISLNDEAVSLDD 260
           || | ||||  : ||||:|| |||| || |:|| ||||||||||| |||| ::   |||
Db     121 KDTPPPVTVPTSSLNWKKLDRSLLFLEAPASGEASLLSEGLRESLSSYISLAED--PLDD 178

Qy     261 A 261
           |
Db     179 A 179


RESULT 7
Q8QZX8
ID   Q8QZX8      PRELIMINARY;      PRT;   280 AA.
AC   Q8QZX8;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Src-like adapter protein SLAP (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ILS, AND ISS;
RX   MEDLINE=21363810; PubMed=11471062;
RA   Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA   Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT   "High-throughput sequence identification of gene coding variants
RT   within alcohol-related QTLs.";
RL   Mamm. Genome 12:657-663(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ILS, AND ISS;
RA   Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA   Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY079449; AAL87537.1; -.
DR   EMBL; AY079450; AAL87538.1; -.
FT   NON_TER       1      1
FT   NON_TER     280    280
SQ   SEQUENCE   280 AA;  31549 MW;  A05C33BF7FEAD951 CRC64;

  Query Match             36.7%;  Score 495.5;  DB 11;  Length 280;
  Best Local Similarity   43.9%;  Pred. No. 3.7e-37;
  Matches  116;  Conservative   38;  Mismatches   81;  Indels   29;  Gaps    7;

Qy       9 KSLPSPS---LSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT1VSED 65
           ||   ||   ||||         |   |   || |  :|:   :    | || | ::|::
```

```
Db       5 KSTSPPSERPLSSS---------EGLESDFLAV-LTDYPSPDISPPIFRRGEKLRVISDE 54

Qy      66 GDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQT 125
           | ||  :|  :|||  || : ||:| ||||:||| |:|||||  ||    |:|:||||:|
Db      55 GGWWKAISLSTGRESYIPGICVARVYHGWLPEGLGRDKAEELLQLPDTKIGSFMIRESET 114

Qy     126 RRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICC 185
           ::| ||||||       :::|||| | | | |||||||| |: || ||||:|| :||
Db     115 KKGFYSLSVR------HRQVKHYRIFRLPNNWYYISPRLTFQCLEDLVTHYSEVADGLCC 168

Qy     186 LLKEPCVLQR-----AGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATG----EESL 236
           :|  ||: |      : | |      |||:::   :|| :        || |      :|||
Db     169 VLTTPCLAQNIPAPTSHPSPCTSPGSPVTLRQKTFDWKRVSRLQEGSEGAENPLRVDESL 228

Qy     237 LSEGLRESLSFYISL-NDEAVSLD 259
           | |||||:: |:|| |:: | |
Db     229 FSYGLRESIASYLSLTGDDSSSFD 252


RESULT 8
Q60898
ID   Q60898      PRELIMINARY;      PRT;   281 AA.
AC   Q60898;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   SRC-like adapter protein.
GN   SLA OR SLAP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95370243; PubMed=7543898;
RA   Pandey A., Duan H., Dixit V.M.;
RT   "Characterization of a novel Src-like adapter protein that associates
RT   with the Eck receptor tyrosine kinase.";
RL   J. Biol. Chem. 270:19201-19204(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20093985; PubMed=10630289;
RA   Carrier A., Nguyen C., Victorero G., Granjeaud S., Rocha D.,
RA   Bernard K., Miazek A., Ferrier P., Malissen M., Naquet P.,
RA   Malissen B., Jordan B.;
RT   "Differential gene expression in CD3e- and RAG1-deficient thymuses:
RT   definition of a set of genes potentially involved in thymocyte
RT   maturation.";
RL   Immunogenetics 50:255-270(1999).
CC   -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR   EMBL; U29056; AAA82756.1; -.
DR   EMBL; AJ131777; CAB66139.1; -.
DR   HSSP; P16277; 1BLK.
DR   MGD; MGI:104295; Sla.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   SH3 domain.
SQ   SEQUENCE   281 AA;  31680 MW;  B34792I656A74DA1 CRC64;

  Query Match             36.7%;  Score 495.5;  DB 1I;  Length 281;
  Best Local Similarity   43.9%;  Pred. No. 3.8e-37;
  Matches  116;  Conservative   38;  Mismatches   81;  Indels   29;  Gaps    7;

Qy       9 KSLPSPS---LSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSED 65
           ||   ||   ||||         |   |   || |  :|:   :    | || | ::|::
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```
Db      6 KSTSPPSERPLSSS---------EGLESDFLAV-LTDYPSPDISPPIFRRGEKLRVISDE 55

Qy     66 GDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQT 125
          | ||  :|  :||| || : ||:| ||||:||| |:|||||| ||    |:|:||||:|
Db     56 GGWWKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQLPDTKIGSFMIRESET 115

Qy    126 RRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICC 185
          ::| ||||||        :::|||| | | | |||||||| |: || ||||:|| :||
Db    116 KKGFYSLSVR------HRQVKHYRIFRLPNNWYYISPRLTFQCLEDLVTHYSEVADGLCC 169

Qy    186 LLKEPCVLQR-----AGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATG----EESL 236
          :|  ||: |      : | |      |||:::   :|| :      || |      :|||
Db    170 VLTTPCLAQNIPAPTSHPSPCTSPGSPVTLRQKTFDWKRVSRLQEGSEGAENPLRVDESL 229

Qy    237 LSEGLRESLSFYISL-NDEAVSLD 259
          | |||||:: |:|| |:: | |
Db    230 FSYGLRESIASYLSLTGDDSSSFD 253


RESULT 9
Q13239
ID   QI3239      PRELIMINARY;      PRT;   276 AA.
AC   Q13239;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative SRC-like adapter protein (SLAP) (SRC-like-adapter).
GN   SLAP.
OS   Homo saplens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Prlmates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96423054; PubMed=8825655;
RA   Angrist M., Wells D.E., Chakravarti A., Pandey A.;
RT   "Chromosomal localization of the mouse Src-like adapter protein (Slap)
RT   gene and its putative human homolog SLA.";
RL   Genomics 30:623-625(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Meljerink P.H.S., Zorn G., Bikker H., Bolhuis P.A., Baas F.;
RL   Submltted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Ohtsukl T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,
RA   Miura Y.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Blechschmldt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
RA   Jonge, Rd, Schllhabel M., Wen G., Menzel U., Dette M., Baumgart C.,
RA   Rosenthal A.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RA   Strausberg R.;
RL   Submltted (APR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR   EMBL; U30473; AAC50357.1; -.
DR   EMBL; U44403; AAC27662.1; -.
DR   EMBL; D89077; BAAI3758.1; -.
DR   EMBL; AF305872; AAG17933.1; -.
DR   EMBL; BC007042; AAH07042.1; -.
DR   HSSP; P08631; 3HCK.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   SH3 domain.                                                    ;
SQ   SEQUENCE   276 AA;  31156 MW;  B0FCC7D7B2ECA378 CRC64;

  Query Match            35.9%;  Score 485.5;  DB 4;  Length 276;
  Best Local Similarity  40.7%;  Pred. No. 3e-36;
  Matches  103;  Conservative   43;  Mismatches   84;  Indels   23;  Gaps    4;

Qy      9 KSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDW 68
          || |:|:       : |:             |  :|:   :    | || | ::|::| |
Db      6 KSTPAPA-------ERPLPNPEGLDSDFLAVLSDYPSPDISPPIFRRGEKLRVISDEGGW 58

Qy     69 WTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRG 128
          |  :|  :|||  || : ||:| ||||:||| |:|||||| ||    |:|:||||:|::|
Db     59 WKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQLPDTKVGSFMIRESETKKG 118

Qy    129 SYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLK 188
          ||||||        :::|||| | | | |||||||| |: ||:||||:|| :||:|
Db    119 FYSLSVR------HRQVKHYRIFRLPNNWYYISPRLTFQCLEDLVNHYSEVADGLCCVLT 172

Qy    189 EPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATG-------EESLLSEGL 241
          ||: |       :    |||:::  ::|: :       |    |       :||| | ||
Db    173 TPCLTQSTAAPAVRASSSPVTLRQKTVDWRRVSR---LQEDPEGTENPLGVDESLFSYGL 229

Qy    242 RESLSFYISLNDE 254
          |||:: |:||  |
Db    230 RESIASYLSLTSE 242


RESULT 10
Q9DDK6
ID   Q9DDK6      PRELIMINARY;      PRT;   502 AA.
AC   Q9DDK6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Src-family tyrosine kinase SCK.
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hordvik I., Male R.;
RT   "A leukocyte cDNA of Atlantic salmon encoding a Src-family tyrosine
RT   kinase.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR   EMBL; AF321110; AAG38611.1; -.
DR   HSSP; P08631; 1AD5.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   ProDom; PD000066; SH3; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; SH3 domain; Transferase.
SQ   SEQUENCE   502 AA;  56600 MW;  82DF0D677AA99980 CRC64;

  Query Match             27.4%;  Score 370.5;  DB 13;  Length 502;
  Best Local Similarity   42.4%;  Pred. No. 2.2e-25;
  Matches   81;  Conservative   29;  Mismatches   66;  Indels   15;  Gaps    3;

Qy      15 SLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSE 74
           |   ||   ||        :: |:||  :      :|  : |: | |: | |:||   |
Db      45 STGPSVPSDGP--------ESIAIALYDYEGINEGDLGFKKGDKLKILQESGEWWRAQSI 96

Qy      75 VSGREYNIPSVHVAKVS---HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYS 131
              :|:|  ||| :||  |     | ::|:||: ||  ||  ||  |:|:||:|:| :||||
Db      97 STGQEGFIPSNYVAIDSLETEEWFFKGVSRKDAERQLLASGNKMGSFMIRDSETTKGSYS 156

Qy     132 LSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPC 191
           |||| |    | | ::||:|  ||||  |||||:|| :|| || || :| | :|  |  ||
Db     157 LSVRDSDSQSGDTVKHYKIRTLDNGGFYISPRITFTTLQELVSHYKKLGDGLCQALTSPC 216

Qy     192 VLQRAGPLPGK 202
           :     | | |
Db     217 L----SPKPQK 223


RESULT 11
O13064
ID   O13064      PRELIMINARY;      PRT;   488 AA.
AC   O13064;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrei. 04, Last sequence update)
DT   01-MAR-2002 (TrEMBLrei. 20, Last annotation update)
DE   Lyn protein tyrosine kinase.
GN   LYN.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Fukami Y., Funabiki K., Sato K.;
RT   "Nucleotide sequence of Xenopus Lyn protein tyrosine kinase.";
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR   EMBL; AB003358; BAA20078.1; -.
DR   HSSP; P08631; 1AD5.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   ProDom; PD000066; SH3; 1.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
SQ   SEQUENCE   488 AA;  55794 MW;  B7E70668B6EA92B2 CRC64;

  Query Match             27.1%;  Score 365.5;  DB 13;  Length 488;
  Best Local Similarity   38.8%;  Pred. No. 6.1e-25;
  Matches   83;  Conservative   36;  Mismatches   78;  Indels   17;  Gaps    4;

Qy       1 MGSLPSRR--------KSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELS 52
             || : |:         |: |:    | : || :  : |      :|| :      :||
Db       1 MGCIKSKTDNPRDAMGKNNPASRTPSLLPGQ-KMIQDIEEQGNIVIALYPYQGIHEDDLS 59

Qy      53 LRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVAKV----SHGWLYEGLSREKAEELL 108
             : || | :: | |:||   |  : :|  ||| :||:|    :  | :: |:|: ||  |
Db      60 FKKGEKLKVLEEHGEWWKAKSLSTKKEGFIPSNYVARVNTLETEEWFFKDLTRKDAERQL 119

Qy     109 LLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPS 168
           | |||  |||||||:| :||||||:|   | : | |:||:|  |||  ||||:|| |
Db     120 LAPGNNPGAFLIRESETSKGSYSLSIRDCDPQTGDVIKHYKIRTLDNGGYYISPRITFTS 179

Qy     169 LQALVDHYSELADDICCLLKEPCVLQRAGPLPGK 202
           :  :: || : || :|  | :||      | | |
Db     180 INEMIQHYQKQADGLCRKLDKPCF----SPKPQK 209


RESULT 12
Q9HBI7
ID   Q9HBI7      PRELIMINARY;      PRT;   161 AA.
AC   Q9HBI7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Src-like adapter protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
RA   Jonge, Rd, Schilhabel M.B., Menzel U., Dette M.D., Baumgart C.,
RA   Jahn N., Rosenthal A.;
RT   "Chromosome 8 genomic sequence.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Genome Sequencing Center Jena;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR   EMBL; AF235100; AAG29878.1; -.
DR   HSSP; P08631; 3HCK.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   ProDom; PD000093; SH2; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   SH3 domain.
FT   NON_TER     161    161
SQ   SEQUENCE   161 AA;  18493 MW;  FC285466804E5B20 CRC64;

  Query Match             26.8%;  Score 362.5;  DB 4;  Length 161;
  Best Local Similarity   44.4%;  Pred. No. 2.5e-25;
  Matches   75;  Conservative   27;  Mismatches   54;  Indels   13;  Gaps    2;

Qy       9 KSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDW 68
             || |:|:       : |:             |  :|:   :    | || | ::|::| |
Db       6 KSTPAPA-------ERPLPNPEGLDSDFLAVLSDYPSPDISPPIFRRGEKLRVISDEGGW 58

Qy      69 WTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRG 128
           |  :|  :|||  || : ||:| ||||:||| |:|||||| ||    |:|:|||||:|::|
Db      59 WKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQLPDTKVGSFMIRESETKKG 118
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Qy    129 SYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYS 177
          ||||||        :::|||||  | | | ||||||||  |: ||:|||
Db    119 FYSLSVR------HRQVKHYRIFRLPNNWYYISPRLTFQCLEDLVNHYS 161


RESULT 13
Q96IN1
ID   Q96IN1      PRELIMINARY;      PRT;   505 AA.
AC   Q96IN1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Unknown (protein for MGC:16168).
OS   Homo saplens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC007371; AAH07371.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   ProDom; PD000066; SH3; 1.
DR   ProDom; PD000093; SH2; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Transferase.
SQ   SEQUENCE   505 AA;  57706 MW;  B5F739BEF8389176 CRC64;

  Query Match           26.4%;  Score 356.5;  DB 4;  Length 505;
  Best Local Similarity 44.2%;  Pred. No. 4.3e-24;
  Matches  76;  Conservative  24;  Mismatches  67;  Indels  5;  Gaps  2;

Qy     25 PVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPS 84
          |     :  |  |||  : |    :( :  || | ::   ||||   | |:|||  :||
Db     51 PPDEHLDEDKHFVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARSLVTGREGYVPS 110

Qy     85 VHVAKVS----HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPA 140
            ||:|       | :    |::||  || | |  |:|||||:| :|:::||||:
Db    111 NFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLIRESETNKGAFSLSVK-DVTT 169

Qy    141 SWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCV 192
          : |:||:| ||| |  |||||:||||||||| |||:  | :|  |  |||
Db    170 QGELIKHYKIRCLDEGGYYISPRITFPSLQALVQHYSKKGDGLCQRLTLPCV 221


RESULT 14
Q95M32
ID   Q95M32      PRELIMINARY;      PRT;   509 AA.
AC   Q95M32;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Lck protein.
GN   LCK.
OS   Hylobates sp. (gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Prlmates; Catarrhlni; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9581;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Picard C.;
RL   Thesis (2001), Department of Experimental Oncology laboratory, U.
DR   EMBL; AJ320182; CAC44027.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   ProDom; PD000066; SH3; 1.
DR   ProDom; PD000093; SH2; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Transferase.
SQ   SEQUENCE   509 AA;  57946 MW;  F1BFE5C237C8DB7E CRC64;

  Query Match           25.5%;  Score 344;  DB 6;  Length 509;
  Best Local Similarity 41.1%;  Pred. No. 6e-23;
  Matches  74;  Conservative  26;  Mismatches  70;  Indels  10;  Gaps  2;

Qy     26 VTMEAERSKAT------AVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGRE 79
          || |      |:       :|| |:       :|    || | |: : |:||   |  :|:|
Db     49 VTYEGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQE 108

Qy     80 YNIPSVHVAKVS----HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVR 135
            ||   ||| :       | :: |||: ||  || |||  |:|||||::  ||:|||||
Db    109 GFIPFNFVAKANSLEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVR 168

Qy    136 LSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQR 195
             : ::||:|  ||||  |||||:||| |  || ||:  :| :|  |  ||  |:
Db    169 DFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQK 228


RESULT 15
Q91X65
ID   Q91X65      PRELIMINARY;      PRT;   509 AA.
AC   Q91X65;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to lymphocyte-specific protein tyrosine kinase.
GN   LCK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SALIVARY GLAND;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011474; AAH11474.1; -.
DR   MGD; MGI:96756; Lck.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   ProDom; PD000066; SH3; 1.
DR   ProDom; PD000093; SH2; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   ATP-binding; Kinase; Transferase.
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SQ SEQUENCE 509 AA; 57942 MW; 3513102F49A7FD0B CRC64;

Query Match 25.4%; Score 342.5; DB 11; Length 509;
Best Local Similarity 39.6%; Pred. No. 8.2e-23;
Matches 78; Conservative 28; Mismatches 84; Indels 7; Gaps 2;

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Qy       3 SLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIV 62
           ||| |  |      |   | :| :   :       :|| |:      :|    || | |:
Db      35 SLPIRNGSEVRDPL---VTYEGSLPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRIL 91

Qy      63 SEDGDWWTVLSEVSGREYNIPSVHVAKVS----HGWLYEGLSREKAEELLLLPGNPGGAF 118
             : |:||   |  :|:|  ||  ||| :      | :: |||: ||  || |||  |:|
Db      92 EQSGEWWKAQSLTTGQEGFIPFNFVAKANSLEPEPWFFKNLSRKDAERQLLAPGNTHGSF 151

Qy     119 LIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYlSPRLTFPSLQALVDHYSE 178
           |||||::  ||:|||||       : ::||:|  ||||  |||||:||| |  || ||:
Db     152 LIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHDLVRHYTN 211

Qy     179 LADDICCLLKEPCVLQR 195
             :| :|  |  ||  |:
Db     212 ASDGLCTKLSRPCQTQK 228
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Search completed: March 24, 2003, 15:50:32
Job time : 46.8955 secs